Claims

1. A method for classification of cancer in an individual having contracted cancer comprising
   i) in a sample from the individual having contracted cancer determining the microsatellite status of the tumor and
   ii) in a sample from the individual having contracted cancer, said sample comprising a plurality of gene expression products the presence and/or amount which forms a pattern, determining from said pattern a prognostic marker, wherein the microsatellite status and the prognostic marker is determined simultaneously or sequentially
   iii) classifying said cancer from the microsatellite status and the prognostic marker.

2. The method according to claim 1, wherein the prognostic marker is the hereditary or sporadic nature of said cancer the determination of which comprises the steps of
   i) in a sample from the individual having contracted cancer, said sample comprising a plurality of gene expression products the presence and/or amount of which forms a pattern that is indicative of the hereditary or sporadic nature of said cancer
   ii) determining the presence and/or amount of said gene expression products forming said pattern,
   iii) obtaining an indication of the hereditary or sporadic nature of said cancer in the individual based on step ii).

3. The method of claims 1 or 2, wherein the determination of microsatellite status comprises the steps of
   i) in a sample from the individual having contracted cancer, said sample comprising a plurality of gene expression products the presence and/or amount of which forms a pattern that is indicative of the microsatellite status of said cancer,
   ii) determining the presence and/or amount of said gene expression products forming said pattern,

iii) obtaining an indication of the microsatellite status of said cancer in the individual based on step ii).

4. The method according to claims 1, 2 or 3, wherein the cancer is colon cancer.

5. The method of any of the preceding claims, wherein a plurality of gene expression products are analysed using solid support, having binding partners (hybridisation partners) for said plurality of gene expression products forming a pattern.

6. The method of any of the preceding claims, wherein a plurality of gene expression products are analysed using binding partners (hybridisation partners) for said plurality of gene expression products forming a pattern.

7. The method of claims 1,2 or 3, wherein at least two of said plurality of gene expression products forming a pattern are used to determine said microsatellite status are selected individually from a group of genes indicative of microsatellite status.

8. The method of claims 1, 2 or 3, wherein at least two of said plurality of gene expression products used to determine the hereditary or sporadic nature of said colon cancer are selected individually from a group of genes indicative for the hereditary or sporadic nature of the cancer.

9. The method of claims 1, 2 or 3, wherein at least two of said plurality of gene expression products forming a pattern used to determine said microsatellite status are selected individually from the group consisting of the genes listed below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
chemokine (C-C motif) ligand 5	NM_002985	CCL5	1
Tryptophanyl-tRNA synthetase	NM_004184	WARS	2
Proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	NM_006263	PSME1	3
Bone marrow stromal cell antigen 2	NM_004335	BST2	4
ubiquitin-conjugating enzyme E2L 6	NM_004223	UBE2L6	5

A kinase (PRKA) anchor protein 1	NM_003488	AKAP1	6
Proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	NM_002818	PSME2	7
carcinoembryonic antigen-related cell adhesion molecule 5	NM_004363	CEACAM5	8
FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	NM_005766	FARP1	9
myosin X	NM_012334	MYO10	10
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11
Autocrine motility factor receptor	NM_001144	AMFR	12
dimethylarginine dimethylaminohydrolase 2	NM_013974	DDAH2	13
tumor necrosis factor, alpha-induced protein 2	NM_006291	TNFAIP2	14
mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	NM_000249	MLH1	15
thymidylate synthetase	NM_001071	TYMS	16
intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	NM_000201	ICAM1	17
general transcription factor IIA, 2, 12kDa	NM_004492	GTF2A2	18
Rho-associated, coiled-coil containing protein kinase 2	NM_004850	ROCK2	19
ATP binding protein associated with cell differentiation	NM_005783	TXNDC9	20
NCK adaptor protein 2	NM_003581	NCK2	21
phytanoyl-CoA hydroxylase (Refsum disease)	NM_006214	PHYH	22
metastais-associated gene family, member 2	NM_004739	MTA2	23
amiloride binding protein 1 (amine oxidase (copper-containing))	NM_001091	ABP1	24
Biliverdin reductase A	NM_000712	BLVRA	25
phospholipase C, beta 4	NM_000933	PLCB4	26
chemokine (C-X-C motif) ligand 9	NM_002416	CXCL9	27
purine-rich element binding protein A	NM_005859	PURA	28
quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating))	NM_014298	QPRT	29
retinoic acid receptor responder (tazarotene induced) 3	NM_004585	RARRES3	30
chemokine (C-C motif) ligand 4	NM_002984	CCL4	31
forkhead box O3A	NM_001455	FOXO3A	32
interferon, alpha-inducible protein (clone IFI-6-16)	NM_002038	G1P3	34
	NM_022873		123
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
	NM_005950	MT1G	36
metallothionein 1G	NM_005950		
tumor necrosis factor receptor superfamily, member 6	NM_000043	TNFRSF6	37
	NM_152877		133
	NM_152876		132
	NM_152875		134
	NM_152872		130
	NM_152873		33
	NM_152871		129

	NM_152874		131
endothelial cell growth factor 1 (platelet-derived)	NM_001953	ECGF1	38
SCO cytochrome oxidase deficient homolog 2 (yeast)	NM_005138	SCO2	39
chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	NM_006419	CXCL13	40
Granulysin	NM_006433	GNLY	41
CD2 antigen (p50), sheep red blood cell receptor	NM_001767	CD2	42
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43
Teratocarcinoma-derived growth factor 1	NM_003212	TDGF1	44
metallothionein 1H	NM_005951	MT1H	45
cytochrome P450, family 2, subfamily B, polypeptide 6	NM_000767	CYP2B6	46
tumor necrosis factor (ligand) superfamily, member 9	NM_003811	TNFSF9	47
RNA binding motif protein 12	NM_006047 NM_006047	RBM12	48
heat shock 105kDa/110kDa protein 1	NM_006644	HSPH1	49
staufen, RNA binding protein (Drosophila)	NM_004602 NM_017452 NM_017453	STAU	50 125 126
lymphocyte antigen 6 complex, locus G6D	NM_021246	LY6G6D	51
calcium binding protein P22	NM_007236	CHP	52
CDC14 cell division cycle 14 homolog B (S. cerevisiae)	NM_003671 NM_033331	CDC14B	53 115
Epiplakin 1	XM_372063	EPPK1	54
metallothionein 1X	NM_005952	MT1X	55
Transforming growth factor, beta receptor II (70/80kDa)	NM_003242	TGFBR2	56
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
Transmembrane 4 superfamily member 6	NM_003270	TM4SF6	58
pleckstrin homology domain containing, family B (evectins) member 1	NM_021200	PLEKHB1	59
apolipoprotein L, 1	NM_003661 NM_145343	APOL1	60 120
Indoleamine-pyrrole 2,3 dioxygenase	NM_002164	INDO	61

forkhead box A2	NM_021784	FOXA2	62
granzyme H (cathepsin G-like 2, protein h-CCPX)	NM_033423	GZMH	63
baculoviral IAP repeat-containing 3	NM_001165	BIRC3	64
Homo sapiens metallothionein 1H-like protein		AF333388 (Hs 382039)	135
KIAA0182 protein	NM_014615	KIAA0182	117
G protein-coupled receptor 56	NM_005682	GPR56	65
	NM_201524		116
metallothionein 2A	NM_005953	MT2A	66
F-box only protein 21	NM_015002	FBXO21	67
erythrocyte membrane protein band 4.1-like 1	NM_012156, NM_012156	EPB41L1	68
hypothetical protein MGC21416	NM_173834	MGC21416	69
protein O-fucosyltransferase 1	NM_015352, NM_015352	POFUT1	70
metallothionein 1E (functional)	NM_175617	MT1E	71
troponin T1, skeletal, slow	NM_003283	TNNT1	72
chimerin (chimaerin) 2	NM_004067	CHN2	73
heterogeneous nuclear ribonucleoprotein H1 (H)	NM_005520	HNRPH1	74
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle	NM_004046	ATP5A1	75
eukaryotic translation initiation factor 5A	NM_001970	EIF5A	76
perforin 1 (pore forming protein)	NM_005041	PRF1	77
OGT(O-Glc-NAc transferase)-interacting protein 106 KDa	NM_014965	OIP106	78
DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	NM_017895	DDX27	79
vacuolar protein sorting 35 (yeast)	NM_018206	VPS35	80
tripartite motif-containing 44	NM_017583	TRIM44	81
transmembrane, prostate androgen induced	NM_020182	TMEPAI	82
RNA	NM_199169		127
	NM_199170		128
dynein, cytoplasmic, light polypeptide 2A	NM_014183	DNCL2A	83
	NM_177953		122
leucine aminopeptidase 3	NM_015907	LAP3	84
Chromosome 20 open reading frame 35	NM_018478	C20orf35	85
	NM_033542		118
solute carrier family 38, member 1	NM_030674	SLC38A1	86

CGI-85 protein	NM_016028	CGI-85	87
death associated transcription factor 1	NM_022105, NM_080796	DATF1	88 121
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
sestrin 1	NM_014454	SESN1	90
hypothetical protein FLJ20315	NM_017763	FLJ20315	91
hypothetical protein FLJ20647	NM_017918	FLJ20647	92
membrane protein expressed in epithelial-like lung adenocarcinoma	NM_024792	CT120	93
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	NM_014314	RIG-I	94
keratin 23 (histone deacetylase inducible)	NM_015515,	KRT23	95
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	NM_007210	GALNT6	96
aryl hydrocarbon receptor nuclear translocator-like 2	NM_020183	ARNTL2	97
apobec-1 complementation factor	NM_014576, NM_138932	ACF	98 119
hypothetical protein FLJ20232	NM_019008	FLJ20232	99
apolipoprotein L, 2	NM_030882, NM_145343	APOL2	100 120
mitochondrial solute carrier protein	NM_016612	MSCP	101
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

10. The method of claims 1, 2 or 3, wherein at least two of said plurality of gene expression products forming a pattern used to determine said microsatellite status are selected individually from the group consisting of the genes listed below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11
metastais-associated gene family, member 2	NM_004739	MTA2	23
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43

protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

11. The method of claims 1, 2 or 3, wherein at least two of said plurality of gene expression products forming a pattern used to determine said microsatellite status are selected individually from the group consisting of the genes listed below

Gene name	Ref seq	Gene symbol	SEQ NO.:	ID
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11	
metastais-associated gene family, member 2	NM_004739	MTA2	23	
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35	
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43	
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124	
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89	
hypothetical protein FLJ20618	NM_017903	FLJ20618	102	
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103	
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104	

12. The method of claims 1, 2 or 3, wherein

i) at least one of said plurality of gene expression products forming a pattern used to determine said microsatellite status is selected from the group of genes consisting of

Gene name	Ref seq	Gene symbol	SEQ NO.:	ID
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11	
metastais-associated gene family, member 2	NM_004739	MTA2	23	

Chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43

and

ii) at least one of said plurality of gene expression products forming a pattern used to determine said microsatellite status is selected from the group of genes consisting of

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

13. The method of claims 1, 2 or 3, wherein

i) at least one of said plurality of gene expression products forming a pattern used to determine said microsatellite status is selected from the group of genes that are down regulated in MSS colon cancers compared to MSI colon cancers consisting of

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11
metastais-associated gene family, member 2	NM_004739	MTA2	23
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
Splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43

and

ii) at least one of said plurality of gene expression products forming a pattern used to determine said microsatellite status is selected from

the group of genes that are up regulated in MSS colon cancers compared to MSI colon cancers consisting of

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

14. The method of claim 13, wherein the difference in the level of the gene expression products forming a pattern is at least one-fold.

15. The method of claim 13, wherein the difference of the level of the gene expression products forming a pattern is at least 1.5 fold.

16. The method of claim 1, 2 or 3, wherein at least one of said plurality of gene expression products used to determine the hereditary or sporadic nature of said colon cancer are selected individually from the group consisting of the genes as listed below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
Homeo box C6	NM_004503	HOXC6	105
Piwi – like 1	NM_004764.2	PIWIL1	106
Mut L homolog 1	NM_00249.2	MLH1	107
Collapsin response mediator protein 1	NM_001313.2	CRMP1	108
Homeo box B2	NM_002145.2	HOXB2	109
Pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyd synthetase)	NM_002860.2	PYCS/ADH18 A1	110
TGFB inducible early growth response	NM_005655.1	TIEG	111
Checkpoint with forkhead and ring finger domains ??	NM_018223.1	CHFR	112
Hypothetical protein FLJ13842	NM_024645.1	FLJ13842	113
Phosphoprotein regulated by mitogenic pathways	NM_025195.1	C8FW	114

17. The method of claim 1, 2 or 3, wherein at least two of said plurality of gene expression products forming a pattern used to determine said hereditary or sporadic nature of colon cancer are the two genes as listed below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
Piwi – like 1	NM_004764.2	PIWIL1	106
Mut L homolog 1	NM_00249.2	MLH1	107

18. The method according to claims 1, 2 or 3, wherein the microsatellite status in an individual having contracted colon cancer is microsatellite instable.

19. The method according to any of the preceding claims, wherein said colon cancer is of Duke's B or Duke's C stage.

20. The method according to any of the preceding claims, wherein said colon cancer is an adenocarcinoma, a carcinoma, a teratoma, a sarcoma, and/or a lymphoma.

21. The method according to any of the preceding claims, wherein the sample is a biopsy of the tissue.

22. The method according to any of the preceding claims, wherein the sample is a cell suspension made from the tissue.

23. The method according to any of the preceding claims, wherein the expression level is determined by determining mRNA of the sample.

24. The method according to any of the preceding claims, wherein the expression level is determined by determining expression products, such as peptides and/or protein in the sample.

25. The method according to any of the preceding claims, wherein the microsatellite status of the colon cancer in an individual has been determined prior to the determination of the presence and/or amount of gene expression products

26. The method according to any of the preceding claims, wherein the sporadic or hereditary nature of a colon cancer has been determined prior to the determination of the presence and/or amount of gene expression products.

27. A method for classification of cancer in an individual having contracted cancer, wherein the microsatellite status is determined by a method comprising the steps of

i) in a sample from the individual having contracted cancer, said sample comprising a plurality of gene expression products the presence and/or amount of which forms a pattern that is indicative of the microsatellite status of said cancer,

ii) determining the presence and/or amount of said gene expression products forming said pattern,

iii) obtaining an indication of the microsatellite status of said cancer in the individual based on step ii).

28. A method for classification of cancer in an individual having contracted cancer, wherein the hereditary or sporadic nature of the cancer is determined by a method comprising the steps of

i) in a sample in a sample from the individual having contracted cancer, said sample comprising a plurality of gene expression products the presence and/or amount of which forms a pattern that is indicative of the hereditary or sporadic nature of said cancer,

ii) determining the presence and/or amount of said gene expression products forming said pattern,

iii) obtaining an indication of the hereditary or sporadic nature of said cancer in the individual based on step ii).

29. The method according to claim 28, wherein the microsatellite status of said cancer is determined simultaneously or sequentially therewith.

30. A method for treatment of an individual comprising the steps of
    i) selecting an individual having contracted a colon cancer, wherein the microsatellite status is stable, determined according to the method of claims 1, 2, 3, 27 or 28
    ii) treating the individual with anti cancer drugs

31. The method of treatment according to claim 30, wherein the anti cancer drug is selected from the group of fluorouracil-based drugs.

32. The method of treatment according to claim 31, wherein the anti cancer drug is selected from 5-fluorouracil, N-methy-N'-nitro-N-nitrosoguanidine and/or 6-thioguanine.

33. The method of treatment according to claim 30, wherein the anti cancer drug is selected from the group of non-fluorouracil based drugs.

34. The method according to claim 33, wherein the anti cancer drug is selected from leucovorin, irrinotecan, oxaliplatin, cetuximab.

35. A method for treatment of an individual comprising the steps of
    i) selecting an individual having contracted a colon cancer, wherein the microsatellite status is instable, determined according to the method of claims 1, 2, 3, 27 or 34
    ii) treating the individual with anti cancer drugs.

36. The method according to claim 35, wherein the anti cancer drug is selected from campothecin or irinotecan.

37. The method according to claim 30 or 35, wherein the microsatellite status has been determined by microsatellite analysis, ELISA, antibody-based histochemical staining, immuno histo chemistry.

38. The method according to claim 30 or 35 wherein the sporadic or hereditary nature of colon cancer has been examined prior to determining the sporadic or hereditary nature of colon cancer by gene expression products forming a pattern.

39. The method according to claim 30 or 35 wherein the sporadic or hereditary nature of colon cancer has been examined by histological examination of the sample.

40. The method according to claim 30 or 35 wherein the sporadic or hereditary nature of colon cancer has been examined by genotyping the sample.

41. A method for reducing malignancy of a cell, said method comprising contacting a tumor cell in question with at least one peptide expressed by at least one gene selected from genes being expressed in an at least two-fold higher in tumor cells than the amount expressed in said tumor cell in question.

42. The method according to claim 41, wherein the at least one peptide is selected individually from genes comprising a sequence as identified below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11
metastais-associated gene family, member 2	NM_004739	MTA2	23
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43

43. The method according to claim 41, wherein the at least one peptide is selected individually from genes comprising a sequence as identified below

Gene name	Ref seq	Gene	SEQ ID

		symbol	NO.:
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

44. The method according to claim 41 or 42, wherein the tumor cell is contacted with at least two different peptides.

45. A method for reducing malignancy of a tumor cell in question comprising,
   i) obtaining at least one gene selected from genes being expressed in at least one fold higher in tumor cells than the amount expressed in the tumor cell in question,
   ii) introducing said at least one gene into the tumor cell in question in a manner allowing expression of said gene(s).

46. The method according to claim 45, wherein the at least one gene is selected from genes comprising a sequence as identified below

Gene name	Ref seq	Gene symbol	SEQ NO.:	ID
Heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11	
metastais-associated gene family, member 2	NM_004739	MTA2	23	
Chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35	
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43	

47. The method according to claim 45, wherein the at least one gene is selected from genes comprising a sequence as identified below

Gene name	Ref seq	Gene symbol	SEQ NO.:	ID
Protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 129	
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89	
hypothetical protein FLJ20618	NM_017903	FLJ20618	102	

SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

48. The method according to claim 45, 46 or 47, wherein at least two different genes are introduced into the tumor cell.

49. A method for reducing malignancy of a cell in question, said method comprising

obtaining at least one nucleotide probe capable of hybridising with at least one gene of a tumor cell in question, said at least one gene being selected from genes being expressed in an amount at least one-fold lower in tumor cells than the amount expressed in said tumor cell in question, and

introducing said at least one nucleotide probe into the tumor cell in question in a manner allowing the probe to hybridise to the at least one gene, thereby inhibiting expression of said at least one gene.

50. The method according to claim 49, wherein the nucleotide probe is selected from probes capable of hybridising to a nucleotide sequence comprising a sequence as identified below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
protein kinase C binding protein 1	NM_012408 NM_183047	PRKCBP1	57 124
hepatocellular carcinoma-associated antigen 112	NM_018487	HCA112	89
hypothetical protein FLJ20618	NM_017903	FLJ20618	102
SET translocation (myeloid leukaemia-associated)	NM_003011.1	SET	103
ATPase, class II, type 9a	Xm_030577.9	ATP9a	104

51. The method according to claim 46, wherein the nucleotide probe is selected from probes capable of hybridising to a nucleotide sequence comprising a sequence as identified below

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
heterogeneous nuclear ribonucleoprotein L	NM_001533	HNRPL	11
metastais-associated gene family, member 2	NM_004739	MTA2	23
chemokine (C-X-C motif) ligand 10	NM_001565	CXCL10	35
splicing factor, arginine/serine-rich 6	NM_006275	SFRS6	43

52. The method according to claim 49, 50 or 51, wherein at least two different probes are introduced into the tumor cell.

53. A method for producing antibodies against an expression product of a cell from a biological tissue, said method comprising the steps of

obtaining expression product(s) from at least one gene said gene being expressed as defined in any of claims 1-29,

immunising a mammal with said expression product(s) obtaining antibodies against the expression product.

54. A method for treatment of an individual comprising the steps of

i) selecting an individual having contracted a colon cancer, wherein the microsatellite status is stable, determined according to the method of claims 1, 2, 3, 27 or 28 and wherein the hereditary nature of said cancer has been determined according to the method of claims 1, 2 or 3

ii) introducing at least one gene into the tumor cell in a manner allowing expression of said gene(s).

55. The method according to claim 54, wherein the at least one gene is selected from MSH2, MLH1, PMS1, PMS2 or MSH6.

Gene name	Ref seq	Gene symbol	SEQ ID NO.:
Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	NM_000251	MSH2	136
Mut L homolog 1	NM_00249.2	MLH1	107
Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	NM_000534	PMS1	137
Homo sapiens PMS2 postmeiotic segregation increased 2 (S. cerevisiae) (PMS2), mRNA	NM_000535	PMS2	138
Homo sapiens mutS homolog 6 (E. coli)	NM_000179	MSH6	139

56. The method according to claim 54 or 55, wherein at least two different genes are introduced.

57. Pharmaceutical composition for the treatment of a classified cancer comprising at least one antibody as defined in claim 53.

58. Pharmaceutical composition for the treatment of a classified cancer comprising at least one polypeptide as defined in any of the claims 41-44.

59. Pharmaceutical composition for the treatment of a classified cancer comprising at least one nucleic acid and/or probe as defined in any of the claims 45-52.

60. The use of a method as defined in any of claims 1- 37 for producing an assay for classifying cancer in animal tissue.

61. The use of a peptide as defined in any of claims 41-44 for preparation of a pharmaceutical composition for the treatment of a cancer in animal tissue.

62. The use of a gene as defined in any of claims 45-52 for preparation of a pharmaceutical composition for the treatment of cancer in animal tissue.

63. The use of a probe as defined in any of claims 49-52 for preparation of a pharmaceutical composition for the treatment of cancer in animal tissue.

64. An assay for classification of cancer in an individual having contracted cancer, comprising

at least one marker capable of determining the microsatellite status in a sample and

at least one marker in a sample determining the prognostic marker, wherein the microsatellite status and the prognostic marker is determined simultaneously or sequentially.

65. The assay according to claim 64, wherein the marker is a nucleotide probe.

66. The assay according to claim 64, wherein the marker is an antibody.

67. The assay according to claim 64, wherein the genes are as defined in any of claims 9-13 or 16-17.